

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2003, 08:52:11 ; Search time 43 Seconds

(without alignments)
991.901 Million cell updates/sec

Title: US-09-836-960-5

Perfect score: 1097

Sequence: 1 MYSAPSACTCCLHFLLCF.....PKYTTVTKRSRRIRTPHPA 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvitus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	95.0	207	13	Q91950 gallus galli
2	363	53.1	210	13	057341 brachydanto
3	578	52.7	208	13	Q90XQ4 ambystoma m
4	578	52.7	212	13	Q9DE51 ambystoma m
5	576	52.5	210	13	042278 brachydanto
6	574	52.3	204	13	Q90696 gallus galli
7	556.5	50.7	200	13	P79925 xenopus lae
8	520.5	47.4	182	13	Q9PT78 oryzias lat
9	406	37.0	181	13	Q90Y80 lampetra ja
10	292	26.6	82	6	062682 canis fami
11	244	22.2	86	13	P79685 ambystoma m
12	234	21.3	80	13	Q90XQ0 ambystoma m
13	197.5	18.0	350	5	Q95IK8 ciona savig
14	181	16.5	208	13	Q9PXY1 xenopus lae
15	177	16.1	186	6	Q95LA7 mustela vis
16	173	15.8	185	11	Q9ERN5 rattus norv

17	171	15.6	191	13	Q9DFC9	09dfc9 brachydanto
18	171	15.6	208	6	Q95LI2	Q95LI2 sus scrofa
19	164	14.9	212	11	Q9EST9	Q9EST9 rattus norv
20	163.5	14.9	214	13	Q90XQ5	Q90XQ5 ambystoma m
21	163.5	14.9	207	11	Q9ER05	Q9ER05 mus musculus
22	163	14.9	212	11	Q9ESL9	Q9ESL9 mus musculus
23	162	14.8	208	6	Q95K97	Q95K97 macaca fasc
24	160.5	14.6	196	13	Q9YH31	Q9YH31 notophthalm
25	160.5	14.6	207	11	Q9ESL8	Q9ESL8 mus musculus
26	159	14.5	195	11	Q9RSJ6	Q9RSJ6 rattus norv
27	158.5	14.4	130	6	077767	077767 canis fami
28	157	14.3	208	4	Q96P59	Q96P59 homo sapien
29	155.5	14.2	155	13	Q90FR9	Q90FR9 fuqu rubrip
30	153.5	14.0	213	6	Q9NIB9	Q9NIB9 ovis aries
31	153	13.9	108	6	Q9NIS7	Q9NIS7 capreolus c
32	153	13.9	192	11	Q9ERW3	Q9ERW3 rattus norv
33	153	13.9	245	11	Q8VCY9	Q8VCY9 mus musculus
34	153	13.9	245	13	Q9W6A2	Q9W6A2 gallus galli
35	151.5	13.8	206	13	Q9YGD8	Q9YGD8 oncorhynch
36	151.5	13.8	212	13	042407	042407 gallus galli
37	151	13.8	153	11	Q925A3	Q925A3 mus musculus
38	150.5	13.7	155	13	Q90Y92	Q90Y92 cynops pyrr
39	150	13.7	199	13	Q91A13	Q91A13 gallus galli
40	149.5	13.6	125	13	Q98TD8	Q98TD8 cynops pyrr
41	148.5	13.5	111	13	Q90XQ1	Q90XQ1 ambystoma m
42	148	13.5	301	5	Q9TRA3	Q9TRA3 ciona savig
43	147	13.4	208	11	Q9RSJ5	Q9RSJ5 rattus norv
44	146.5	13.4	196	4	P78443	P78443 homo sapien
45	145.5	13.3	106	6	Q9NIS8	Q9NIS8 capreolus c

ALIGNMENTS

RESULT 1
ID Q91950 PRELIMINARY: PRT: 207 AA.
AC Q91950;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FGF-18.
GN FGF-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20368156; PubMed-10906450;
RA Ohuchi H., Kimura S., Watanabe M., Itoh N.;
RT "Involvement of fibroblast growth factor (FGF)18-FGF8 signaling in
RT specification of left-right asymmetry and brain and limb development
RT of the chick embryo.";
RL Mech. Dev. 95:55-66(2000).

DR EMBL: AB030229; BAB9537.1; -;
DR HSSP: P3137L; IG82;
DR InterPro: IPR002209; HB/F-growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF_1.
DR PRINTS: PRO0262; IL1HBGF.
DR PRODom: PD000831; HB/F-growthfact; 1.
DR SMART: SM00442; FGF_1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOWN_1.
DR SPOUDNCE 207 AA; 24052 MW; 1DB6C82F266C1 CRC64;
SQ

Query Match 95.0%; Score 1042; DB 13; Length 207;
Best Local Similarity 94.2%; Pred. No. 2e-87;
Matches 195; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MYSAPSACTCCLHFLLCFQYOVVLAENVDFRIHENOTRRADVDVSRQQLRYOYSR 60
||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db      1 MSLSACTCLHLLCFQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSR 60
Oy      61 TSGKHIVLGRISARGEDGDKYAQLLVETDFGSOVRIGKETEFEYLCMNRKGLVGR 120
        61 TSGKHIVLGRISARGEDGDKYAQLLVETDFGSOVRIGKETEFEYLCMNRKGLVGR 120
Db      121 DGTSGKECVFIEKLENNYATMSAKYSGWYGFTRKGRPRKGPRTRENOOVHFMKRYPK 180
        121 DGTSGKECVFIEKLENNYATMSAKYSGWYGFTRKGRPRKGPRTRENOOVHFMKRYPK 180
Oy      181 GOPELOKPEKYYTVTKRSRRIRPTHPA 207
        181 GOPELOKPEKYYTVTKRSRRIRPTHPA 207
Db      181 GOPELOKPEKYYTVTKRSRRIRPTHPA 207

RESULT 2
057341 PRELIMINARY: PRT: 210 AA.
ID      057341
AC      057341
DT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8.
GN      FGF8 OR FGF-8 OR FGF8.
OS      Brachydanio rerio (Zebrafish) (Zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96043861; PubMed=9334274;
RA      Fuentehauer M., Thisse C., Thisse B.;
RT      "A role for FGF-8 in the dorsoventral patterning of the zebrafish
RT      gastrula.";
RL      Development 124:4253-4264(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96274197; PubMed=9609821;
RA      Reifers F., Boehl H., Walsh E.C., Crossley P.H., Stanier D.Y.R.,
RA      Brand M.;
RT      "Fgf8 is mutated in zebrafish acerebellar (ace) mutants and is
RT      required for maintenance of midbrain-hindbrain boundary development
RT      and somitogenesis.";
RL      Development 125:2381-2395(1998).
DR      EMBL; AF034264; AAC60303.1; -
DR      EMBL; AF051365; AAC41302.1; -
DR      HSSP; P31371; 1G82.
DR      ZFIN; ZDB-GENE-990415-72; fgf8.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ      SEQUENCE 210 AA; 24697 MW; 9D9CA5B8E18A435A CRC64;

Query Match      53.1%; Score 583; DB 13; Length 210;
Best Local Similarity 55.9%; Pred. No. 1.7e-45;
Matches 113; Conservative 33; Mismatches 48; Indels 8; Gaps 4;
Oy      5 PSACICLHLLCFQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSGK 64
        5 PSRLSYLHLHFAFCYVQVNT-QSPNPTQHVSEOSKVTVSRRLIRTYOLYSRTSGK 63
Db      5 PSRLSYLHLHFAFCYVQVNT-QSPNPTQHVSEOSKVTVSRRLIRTYOLYSRTSGK 63
Oy      65 HVOVL-GRISARGEDGDKYAQLLVETDFGSOVRIGKETEFEYLCMNRKGLVGRPGT 123
        65 HVOVLANKINAMADGDVNAKLVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 123
Db      64 HVOVLANKINAMADGDVNAKLVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 123
Oy      124 SKCEVIEKLENNYATMSAKYSGWYGFTRKGRPRKGPRTRENOOVHFMKRYPK-Q 182
        124 GKDCEFEIVLENNYATLQNVKGYMAFTRKGRPRKGSKTROHOREVHFMKRLPKGH 183
Db      124 GKDCEFEIVLENNYATLQNVKGYMAFTRKGRPRKGSKTROHOREVHFMKRLPKGH 183
Oy      183 PELOKPEKYYTV-----TKRSR 199

```

```

Db      184 IAEHRPDEFINYPFNRRTRR 205
        184 IAEHRPDEFINYPFNRRTRR 205

RESULT 3
090X04 PRELIMINARY: PRT: 208 AA.
ID      090X04
AC      090X04
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8 (Fragment).
OS      Ambystoma mexicanum (Axolotl).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_TaxID=8296;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21439472; PubMed=11555861;
RA      Christensen R.N., Weinstein M., Tassava R.A.;
RT      "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT      and semi-quantitative RT-PCR expression studies.";
RL      J. Exp. Zool. 290:529-540(2001).
DR      EMBL; AF360985; AAL16958.1; -
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 208 AA; 23977 MW; 9D32A77442AB070E CRC64;

Query Match      52.7%; Score 578; DB 13; Length 208;
Best Local Similarity 55.4%; Pred. No. 4.9e-45;
Matches 112; Conservative 34; Mismatches 50; Indels 6; Gaps 3;
Oy      4 APSACTCLHLLCFQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSG 63
        7 ASSVGYLLHLLFVLCMQAKTV-QSPNPTQHVSRQSLVTDQLSRRLIRTYOLYSRPSG 65
Db      7 ASSVGYLLHLLFVLCMQAKTV-QSPNPTQHVSRQSLVTDQLSRRLIRTYOLYSRPSG 65
Oy      64 KHIVLGRISARGEDGDKYAQLLVETDFGSOVRIGKETEFEYLCMNRKGLVGRPG 122
        66 KHIVLGRISARGEDGDKYAQLLVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 125
Db      66 KHIVLGRISARGEDGDKYAQLLVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 125
Oy      123 TSGKECVFIEKLENNYATMSAKYSGWYGFTRKGRPRKGPRTRENOOVHFMKRYPKG- 181
        126 RKDCVFEIVLENNYATLQNVKGYMAFTRKGRPRKGSKTROHOREVHFMKRLPKGH 185
Db      126 RKDCVFEIVLENNYATLQNVKGYMAFTRKGRPRKGSKTROHOREVHFMKRLPKGH 185
Oy      182 ---QPELOKPEKYYTVTKRSRR 200
        186 QTEPHRRPEFVNPFNRRSR 207
Db      186 QTEPHRRPEFVNPFNRRSR 207

RESULT 4
09DE51 PRELIMINARY: PRT: 212 AA.
ID      09DE51
AC      09DE51
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8.
GN      FGF-8.
OS      Ambystoma mexicanum (Axolotl).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_TaxID=8296;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Han M.J., Chung H.M., Nham S.U., Kim W.S.;
RT      "Partial cloning of FGF-8 cDNA in Mexican axolotl, Ambystoma
RT      mexicanum.";

```

RL Hanguk Yujon Hakhoe Chi 19:169-176(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20581706; PubMed=11146506;
 RA Han M.J., An J.Y., Kim W.S.,
 "Expression Patterns of Fgf-8 During Development and Limb Regeneration
 of the Axolotl,"
 RT Dev. Dyn. 220:40-48(2001).
 RL EMBL; AF190448; AAG45674.1; -
 DR HSSP; P31371; I682.
 DR Interpro: IPR002209; HB/F-growthfact.
 DR Interpro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; EGF_1.
 DR PRINTS; PR00263; IL1HBGF.
 DR Prodom: PD000831; HB/F-growthfact; 1.
 DR SMART; SM00442; EGF_1.
 DR PROSITE; PS00247; HBGF_EGF; UNKNOWN_1.
 SO SEQUENCE 212 AA; 24368 MW; B3f7BE03d4210A6A CRC64;

[illegible]

```

RESULT 5
042278
ID 042278 PRELIMINARY; PRT; 210 AA.
AC 042278;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor 8.
FCF8.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Sleptsova-Friedrich I.L., Poon K.L., Clark M., Lehrach R., Korzh V.P.;
RT "FCF8 expression characterizes inductive boundaries in CNS and other
RT tissues of zebrafish."
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF030560; AAB82614.1; -.
DR HSSP; P03371; 1682.
DR InterPro; IPR002209; HB/F_growthfact.
DR Pfam; PF00167; FGF. 1.
DR Prodom; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF. 1.
DR PROSITE; PS00247; HBG_FGF; UNKNOWN_1.
SQ SEQUENCE 210 AA; 24672 MW; EE8665316B7B97E CRC64;

Query March 52.5% Score 576; DB 13; Length 210;
Best Local Similarity 55.0% Pred. No. 7.6e-45;
Matches 111; Conservative 34; Mismatches 49; Indels 8; Gaps 4;

```

[illegible]

RESULT 6			
090696			
ID	Q90696	PRELIMINARY;	PRT; 204 AA.
AC	Q90696;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)		
DE	Fibroblast growth factor 8 FGF8 (fragment).		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE=96140646; PubMed=8548816;		
RA	Crossley P.H., Minowada G., MacArthur C.A., Martin G.R.;		
RT	"Roles for FGF8 in the induction, initiation, and maintenance of chick		
RT	limb development.";		
RL	Cell 84:127-136(1996).		
RL	EMBL; U041467; AA93296.1; -		
DR	HSSP; P31371; IG82.		
DR	InterPro: IPR002209; HB/E-growthfact.		
DR	InterPro: IPR002348; IL1_HBGF.		
DR	Pfam: PF00167; FGF; 1		
DR	PRINTS; PR00262; IL1HBGF.		
DR	ProDom; PD000831; HB/F-growthfact; 1.		
DR	SMART; SM00442; FGF; 1.		
DR	PROSITE; PS00247; HBGF_FGF; 1.		
FT	NON_TER 1 1		
SQ	SEQUENCE 204 AA; 23730 MW; 5C6AC63F72E23D979 CRC64;		

[illegible]

```
ID      P79925      PRELIMINARY;      PRT;      200 AA.
AC      P79925;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Fibroblast growth factor 8 (Fragment).
GN      FGF-8.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC      Xenopodidae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98104248; Pubmed=9441681;
RA      Christen B., Slack J.M.W.;
RT      "FGF-8 is Associated with Anteroposterior Patterning and Limb
RT      Regeneration in Xenopus."
RL      Dev. Biol. 192:455-466(1997).
DR      EMBL; Y10312; CAA71365.1; -.
DR      HSSP; P31371; 1G82.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      InterPro; IPR002348; ILL_HBGF.
DR      Pfam; PF00167; FGF; 1.
DR      PRINTS; PR00262; ILLHBGF.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER      200
FT      SEQUENCE      200 AA; 23453 MM; AB36B51C5ED5C7A CRC64;

Query Match      50.7%; Score 556.5; DB 13; Length 200;
Best Local Similarity 53.8%; Pred. No. 4.3e-43;
Matches 106; Conservative 34; Mismatches 40; Indels 17; Gaps 4;

QY      11 LCHEFLLCFQYQVLYAEVNDYFRHVENOTRRADVRSRQOLRYOLYSTRSGKHIOVL- 69
DB      11 LHLHFLYICQAO-----HYRQSLVTDLQSLRLIRYQLYSTSGKHVILA 58
QY      70 GRRISARGEDGKYAQLLVETDFGSOVRIKGETEFYLCMNRKGLVGPDTGSKCEVF 139
DB      59 NKRINMAEDGDPAKLIVETDFGSRVRIKGAETGYICMNRKGLIGTNGKDCVF 118
QY      130 IEVLENNYATLMSAKSSGYVGFTRKGRPKRPTRENOVDVHFMRKRYKQ--PELQK 167
DB      119 SEVLENNYATLVNRYEGFMAFTRGRGRPKSGKTRQHQREVEHFMKRLPHTTEPHK 178
QY      188 PFKYTT--VTKRSRRIR 202
DB      179 RFEFINPFVRKSRKTR 195

RESULT 8
ID      Q9PT78      PRELIMINARY;      PRT;      182 AA.
AC      Q9PT78;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Fgf8 (Fragment).
OS      Oryzias latipes (Medaka fish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC      Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX      NCBI_TaxID=8090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Carl M., Wiltbrodt J.;
RT      "Graded interference with FGF-signalling uncovers its dorso-ventral
RT      asymmetry at the mid-hindbrain boundary."
RT      Submitted (JUN-1999) to the EMBL/Genbank/DDbJ databases.
EMBL; AJ243210; CAB64349.1; -;
```

```
DR      HSSP; P31371; 1G82.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      InterPro; IPR002348; ILL_HBGF.
DR      Pfam; PF00167; FGF; 1.
DR      PRINTS; PR00262; ILLHBGF.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
FT      NON_TER      1
FT      NON_TER      182
FT      SEQUENCE      182 AA; 20702 MM; 1EF82473824A8DOC CRC64;

Query Match      47.4%; Score 520.5; DB 13; Length 182;
Best Local Similarity 62.8%; Pred. No. 7.5e-40;
Matches 93; Conservative 30; Mismatches 24; Indels 1; Gaps 1;

QY      36 HVENQTRARDDVRSRQOLRYOLYSTSGKHIOVL-GRRISARGEDGKYAQLLVETDFG 94
DB      2 HVRQSVYTHVSRRLRYQLYSTSGKHVQLSNKRINAMAEVDGVAKLIVETDFG 61
QY      95 SOVRIRKGETEFYLCMNRKGLVGPDTGSKCEVFIEKYLENNYATLMSAKSGYVGF 154
DB      62 SOVRIRKAGTGLYICMNRKGLIGTNGKQSRACIFTEIVLENNYATLRNHYNDWYMAFT 121
QY      155 KKGPRKGPRTRENOVDVHFMRKRYKQ 182
DB      122 RRGPRKRSQTRQHQREVEHFMKRLPFRQ 149

RESULT 9
ID      Q90Y80      PRELIMINARY;      PRT;      181 AA.
AC      Q90Y80;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Ljfgf8 (Fragment).
GN      Ljfgf8.
OS      Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC      Petromyzontiformes; Petromyzontidae; Lethenteron.
OX      NCBI_TaxID=94989;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shigetani Y., Sugahara F., Kawakami Y., Hirano S.,
RA      Kuratani S.;
RT      "Shape precedes structure: an exaptation for the vertebrate jaw
RT      evolution."
RT      Submitted (SEP-2001) to the EMBL/Genbank/DDbJ databases.
RL      EMBL; AB071892; BAB68397.1; -.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER      1
FT      NON_TER      181
FT      SEQUENCE      181 AA; 20920 MM; 8F40A6764CE663DC CRC64;

Query Match      37.0%; Score 406; DB 13; Length 181;
Best Local Similarity 57.7%; Pred. No. 2.2e-29;
Matches 75; Conservative 25; Mismatches 28; Indels 2; Gaps 1;

QY      74 SARGEDGDKYAOILVETDFGSOVRIKGETEFYLCMNRKGLVGPDTGSKCEVFIEKY 133
DB      1 NARADGDNKFAKLIVETDFGSRVRIKGAESGYICMNRKGLVGPDTGSKCEVFIEKY 60
QY      134 LENNYATLMSAKSGYVGFTRKGRPKRPTRENOVDVHFMRKRYKGPPELQKPP--KY 191
DB      61 LENNYATLMSVNGYMGFTTRGRPKRSQTSQHQREVEHFMKRLPQRTSEERERFIQYA 120
QY      192 TTYTKRSRRIR 201
DB      121 TGAARSKRM 130
```

RESULT 10

062682 PRELIMINARY; PRT; 82 AA.
AC 062682;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor-8 (Fragment).
GN FGF-8.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Canaan H., Lin Y.C.;
RT "Nucleotide sequence of canine fibroblast growth factor-8 (FGF-8).";
RL In Vitro Cell. Dev. Biol. 34:278-279(1998).
DR EMBL: AF024487; AAC17218.1; -
DR HSSP: P31371; 1G82.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOWN_1.
FT NON_TER 1 1
FT 82 82
SQ SEQUENCE 82 AA; 9226 MW; A22CDAF2A7B27A8 CRC64;

Query Match

Best Local Similarity 26.6%; Score 292; DB 6; Length 82;
Matches 51; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 71 RRSARGEDGDKYQALLVETDTEGSGVRIKGRKTEFYLCNMRKGLVGPDTGSKGVFI 130
Db 2 KRINAMEDDGPFAKLLVETDTEGSRVRVGAETGLYICNMRKGLVGPDTGSKGVFI 61
QY 131 EKVLENNYTLMSAKYSGWYV 151
Db 62 EIELENNYTLQNKAKYEGWYM 82

RESULT 11

P79685 PRELIMINARY; PRT; 86 AA.
AC P79685;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor 8 (Fragment).
GN FGF8.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_Taxid=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Han M.J., Kim W.S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y11093; CAA71967.1; -
DR HSSP: P09038; 1BFG.
DR InterPro: IPR002209; HB/F_growthfact.
DR Pfam: PF00167; FGF; 1.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
FT NON_TER 1 1
FT 86 86
SQ SEQUENCE 86 AA; 10522 MW; 09B38BDB5E2A95C1F CRC64;

Query Match

22.2%; Score 244; DB 13; Length 86;

Best Local Similarity 56.0%; Pred. No. 5.6e-15;
Matches 47; Conservative 13; Mismatches 20; Indels 4; Gaps 1;

QY 127 CVFIEKYLENNYTLMSAKYSGWYVGFTRKGRPRKGPRTRENQODVHMKRYPKG----Q 182
Db 2 CVFSEIVLENNYTLQNKAKYEGWYMAFTRKGRPGSKSTRQHQREVHMKRLPKGHQTE 61
QY 183 PELQKPFYTTVTKRSRRIRPTHP 206
Db 62 PHRRFEVNYPFNRRSKRTRHSP 85

RESULT 12

090X00 PRELIMINARY; PRT; 80 AA.
AC 090X00;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor 8 (Fragment).
OS Ambystoma maculatum (spotted salamander).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OX NCBI_Taxid=43114;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21439472; Pubmed-11555861;
RA Christensen R.N., Weinstein M., Tassava R.A.;
RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning and semi-quantitative RT-PCR expression studies.";
J. Exp. Zool. 290:529-540(2001).
DR EMBL: AF360989; AAL16962.1; -
DR InterPro: IPR002209; HB/F_growthfact.
DR Pfam: PF00167; FGF; 1.
DR ProDom: PD000831; HB/F_growthfact; 1.
FT NON_TER 1 1
FT 80 80
SQ SEQUENCE 80 AA; 9689 MW; 16A5FDA193F5779 CRC64;

Query Match
Best Local Similarity 21.3%; Score 234; DB 13; Length 80;
Matches 45; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 127 CVFIEKYLENNYTLMSAKYSGWYVGFTRKGRPRKGPRTRENQODVHMKRYPKG----Q 182
Db 2 CVFSEIVLENNYTLQNKAKYEGWYMAFTRKGRPGSKSTRQHQREVHMKRLPKGHQTE 61
QY 183 PELQKPFYTTVTKRSRRIRPTHP 200
Db 62 PHRRFEVNYPFNRRSKR 79

RESULT 13

095YK8 PRELIMINARY; PRT; 350 AA.
AC 095YK8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor A.
GN CS-FGA.
OS Clona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCBI_Taxid=51511;
RN [1]
RP SEQUENCE FROM N.A.
RA Satou Y., Imai K.S., Satou N.;
RT "Clona savignyi genes.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB057737; BAB68346.1; -
DR InterPro: IPR002209; HB/F_growthfact.

